

# SEQUENCE LISTING

<110> Panaccio, Michael  
 Rosey, Everett Lee  
 Sinistaj, Meri  
 Hasse, Detlef  
 Parsons, Jim  
 Ankenbauer, Robert G.

<120> LAWSONIA DERIVED GENE AND RELATED FLGE  
 POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES

<130> DAVI150.001APC

<140> US 10/009,823

<141> 2001-11-13

<150> PCT/AU00/00437

<151> 2000-05-11

<150> US 60/133,973

<151> 1999-05-13

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 502

<212> PRT

<213> Lawsonia intracellularis

<400> 1

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		20					25					30			
Gly	Tyr	Lys	Gln	Gln	Gln	Val	Val	Phe	Gln	Asp	Leu	Phe	Ser	Gln	Asp
	35					40					45				
Leu	Ala	Ile	Gly	Ser	Thr	Gly	Ser	Gln	Gly	Pro	Asn	Gln	Ala	Gly	Met
	50				55					60					
Gly	Ala	Gln	Val	Gly	Ser	Val	Arg	Thr	Ile	Phe	Thr	Gln	Gly	Ala	Phe
65				70				75						80	
Glu	Pro	Gly	Asn	Ser	Val	Thr	Asp	Leu	Ala	Ile	Gly	Gly	Lys	Gly	Phe
			85				90					95			
Phe	Gln	Val	Thr	Leu	Glu	Asp	Lys	Val	His	Tyr	Thr	Arg	Ala	Gly	Asn
	100					105						110			
Phe	Arg	Phe	Thr	Gln	Asp	Gly	Phe	Leu	Asn	Asp	Pro	Ser	Gly	Phe	Thr
	115				120					125					
Leu	Met	Gly	Ser	Arg	Ile	Ser	Asn	Asn	Pro	Asn	Ile	Lys	Lys	Glu	Thr
	130				135					140					
Leu	Glu	Pro	Ile	Gln	Leu	Asp	Phe	Asn	Asp	Pro	Thr	Val	Ala	Lys	Ser
145				150						155					160

Pro	Ala	Lys	Thr	Ser	Thr	Ala	Leu	Asn	Ala	Val	Val	Asn	Leu	Gly	Asp	165	170	175
Ser	Thr	Asp	Lys	Thr	Gln	Ser	Glu	Ala	Asn	Pro	Tyr	Phe	Ala	Leu	Leu	180	185	190
Glu	Ser	Trp	Lys	Gly	Asn	Gly	Thr	Pro	Pro	Ile	Ser	Thr	Ser	Asn	Tyr	195	200	205
Ser	Tyr	Ala	Gln	Pro	Met	Arg	Val	Tyr	Asp	Gln	Gln	Gly	Asn	Ser	His	210	215	220
Asp	Ile	Thr	Val	Tyr	Phe	Asp	Gly	Ala	Pro	Ser	Ser	Thr	Gly	Ser	Lys	225	230	235
Thr	Phe	Glu	Tyr	Leu	Val	Ala	Met	Asn	Pro	Ser	Glu	Asp	Gly	Ser	Ala	245	250	255
Ala	Ser	Gly	Thr	Asp	Ser	Ala	Gly	Leu	Leu	Met	Ser	Gly	Thr	Met	Thr	260	265	270
Phe	Ser	Ser	Asn	Gly	Glu	Leu	Lys	Asn	Met	Thr	Ala	Phe	Thr	Pro	Thr	275	280	285
Gly	Ser	Ala	Thr	Lys	Asp	Leu	Asn	Ala	Trp	Gln	Pro	Ala	Pro	Leu	Val	290	295	300
Asn	Gly	Leu	Pro	Gln	Phe	Ser	Ala	Asn	Phe	Val	Gly	Ala	Gly	Ile	Gln	305	310	315
Pro	Leu	Thr	Leu	Asp	Phe	Gly	Ile	Lys	Ser	Gln	Gln	Asn	Met	Trp	Ala	325	330	335
Gly	Ala	Pro	Ala	Ser	Ala	Ala	Ala	Ile	Gly	Thr	Asp	Ile	Gly	Lys	Leu	340	345	350
Pro	Ser	Met	Met	Pro	Ile	Gln	Thr	Ser	Ser	Gly	Asn	Ser	Thr	Ala	Arg	355	360	365
Asn	Gly	Ser	Ser	Ser	Thr	Arg	Arg	Tyr	Ser	Gln	Asp	Gly	Tyr	Pro	Gln	370	375	380
Gly	Asp	Leu	Val	Asp	Val	Thr	Ile	Thr	Ser	Glu	Gly	Lys	Leu	Gln	Gly	385	390	395
Lys	Tyr	Ser	Asn	Ser	Gln	Val	Val	Asp	Phe	Tyr	Asn	Ile	Pro	Leu	Ala	405	410	415
Arg	Phe	Thr	Ser	Glu	Asp	Gly	Leu	Arg	Arg	Glu	Gly	Asn	Asn	His	Tyr	420	425	430
Ser	Ala	Thr	Leu	Asp	Ser	Gly	Gly	Pro	Glu	Phe	Gly	Leu	Pro	Gly	Thr	435	440	445
Ser	Asn	Tyr	Gly	Lys	Leu	Ser	Val	Asn	Gln	Leu	Glu	Thr	Ser	Asn	Val	450	455	460
Asp	Met	Ser	Arg	Glu	Met	Val	Asn	Met	Ile	Ile	Ile	Gln	Arg	Gly	Phe	465	470	475
Gln	Met	Asn	Ser	Lys	Ser	Val	Thr	Thr	Ala	Asp	Thr	Met	Leu	Gln	Lys	485	490	495
Ala	Leu	Glu	Leu	Lys	Arg											500		

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 <212> DNA  
 <213> Lawsonia intracellularis

<220>  
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aca ggg ttg ggt act gtc tcc aat aat att gct aac gca aat acc att	96
Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile	
20 25 30	
ggg tat aag cag caa cag gta gtg ttt caa gac ctg ttt agt caa gat	144
Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp	
35 40 45	
tta gca ata ggt tct act gga agt cag ggg cca aac cag gct ggt atg	192
Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met	
50 55 60	
gga gca cag gtt gga agt gtt cgc aca att ttt aca cag ggt gct ttt	240
Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe	
65 70 75 80	
gaa cct ggc aat agt gta aca gat ctt gct att ggt gga aaa ggt ttt	288
Glu Pro Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe	
85 90 95	
ttt cag gtt aca tta gag gat aaa gta cac tat aca cga gca ggg aat	336
Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn	
100 105 110	
ttt cgt ttt act caa gat ggt ttt tta aat gat cct agc gga ttt act	384
Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr	
115 120 125	
tta atg ggc tca aga ata tct aat aat cct aac ata aaa aag gaa acc	432
Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr	
130 135 140	
ctt gaa cca att cag tta gac ttt aat gat cct aca gta gca aag tct	480
Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser	
145 150 155 160	
cct gca aaa aca agt aca gca tta aac gct gtg gta aac ctt ggt gat	528
Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp	
165 170 175	
agt aca gat aaa aca caa agt gaa gct aat cca tac ttt gca ctt ctt	576
Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu	
180 185 190	
gag agc tgg aaa gga aat gga aca cct cct att tct aca tca aac tac	624
Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr	
195 200 205	
tca tat gca caa cct atg aga gta tat gat caa caa gga aat tct cac	672
Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His	

210	215	220	
gat ata act gta tat ttt gat gga gca ccc tct tca aca gga agt aaa			720
Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys			
225	230	235	240
aca ttt gaa tac ctt gta gct atg aat cct agt gaa gat gga agt gct			768
Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala			
245	250		255
gca tca gga aca gat agt gca ggt ctc tta atg tct gga act atg aca			816
Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr			
260	265		270
ttt tca agt aat ggc gaa tta aaa aat atg aca gct ttt act cct act			864
Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr			
275	280		285
ggc tct gca aca aaa gat tta aat gca tgg caa cca gca cca tta gtc			912
Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val			
290	295		300
aat ggt tta cca cag ttt tca gca aat ttt gtt ggt gca gga ata cag			960
Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln			
305	310		315
cct tta aca tta gac ttt gga att aaa agc caa cag aat atg tgg gca			1008
Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala			
325	330		335
gga gct cca gca tcc gct gct gcc ata ggt aca gat att ggg aaa ttg			1056
Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu			
340	345		350
cca tca atg atg cca ata caa aca tcc agc ggt aat tct aca gca aga			1104
Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg			
355	360		365
aat gga tca tct tca aca aga aga tat agc caa gat ggt tat cct cag			1152
Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln			
370	375		380
gga gat cta gta gat gtc aca att acc tct gaa ggg aaa tta caa ggt			1200
Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly			
385	390		395
aag tat agt aat agt cag gtt gtt gat ttt tat aat att cct tta gca			1248
Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala			
405	410		415
cgc ttt aca agt gag gat gga tta aga cga gaa ggg aat aac cat tat			1296
Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr			
420	425		430
tcc gca aca ctt gac tca ggt ggg cca gag ttt gga ttg cca gga aca			1344

Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr  
 435 440 445

tct aac tat gga aaa ctt agt gtg aat caa ctt gag act tct aac gta 1392  
 Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val  
 450 455 460

gac atg agc aga gaa atg gtt aat atg att att att caa cgt ggt ttt 1440  
 Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe  
 465 470 475 480

cag atg aat agt aaa tct gtt aca aca gca gac aca atg cta caa aaa 1488  
 Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys  
 485 490 495

gca ctt gaa cta aag cgt taa 1509  
 Ala Leu Glu Leu Lys Arg \*  
 500

<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer, RA170.

<400> 3 21  
 ctatttttag gagatgttat c

<210> 4  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer, RA171.

<400> 4 22  
 tacaaaatta acaataaaat ac

<210> 5  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer, FlaF.

<221> misc\_feature  
 <222> (1)...(38)  
 <223> n = A,T,C or G

<400> 5

gcgaattcca tatgatgggg agtttggtta ttgntgcc

38

<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer, FlgE3'.

<400> 6

gctctagaga ctagtcatat taacgcttta gttcaagtgc

40

<210> 7

<211> 477

<212> PRT

<213> Treponema phagedenis

<400> 7

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Gly	Val	Asn	Pro	Lys	Glu	Val	Gly	Leu	Gly	Val	Met	Val	Ala	Ser	Gly
		20						25					30		
Val	Asn	Pro	Lys	Glu	Val	Gly	Leu	Gly	Val	Met	Val	Ala	Ser	Thr	Arg
		35					40					45			
Met	Asp	Val	Ile	Gly	Asn	Asn	Val	Ala	Asn	Val	Asn	Thr	Thr	Gly	Phe
	50				55						60				
Lys	Arg	Gly	Arg	Ile	Asp	Thr	Val	His	Thr	Gln	Gly	Ala	Leu	Gln	Thr
65				70					75					80	
Thr	Gly	Ile	Asn	Thr	Asp	Ile	Ala	Ile	Val	Asn	Phe	Gln	Asp	Leu	Ile
			85					90						95	
Ser	Gln	Gln	Leu	Ser	Gly	Ala	Ser	Arg	Pro	Asn	Glu	Glu	Val	Gly	Gln
		100					105						110		
Gly	Asn	Gly	Phe	Phe	Ile	Leu	Lys	Asp	Gly	Glu	Lys	Ser	Phe	Tyr	Thr
	115					120						125			
Thr	Ala	Gly	Ala	Phe	Gly	Val	Asp	Arg	Asp	Gly	Thr	Leu	Val	Asn	Pro
	130				135						140				
Ala	Asn	Gly	Ala	Cys	Asn	Leu	Asp	Lys	Arg	Leu	Met	Arg	Val	Gln	Gly
145				150					155					160	
Trp	Met	Ala	Glu	Asp	Ile	Glu	Gly	Gln	Gln	Ile	Ile	Asn	Thr	Ser	Asp
			165					170						175	
Gln	Pro	Glu	Leu	Pro	Glu	Gly	Ala	Asn	Gln	Ala	Asp	Ile	Leu	Arg	Ser
		180					185						190		
Thr	Glu	Asp	Leu	Ile	Ile	Pro	Ile	Gly	Gln	Lys	Ile	Asp	Ala	Lys	Ala
	195					200						205			
Thr	Thr	Asp	Val	Ala	Tyr	Thr	Trp	Ala	Thr	Asp	Phe	Asn	Val	Tyr	Asp
	210				215						220				
Thr	Phe	Gly	Glu	Gln	His	Lys	Leu	Gln	Met	Val	Phe	Ser	Arg	Val	Pro
225				230					235					240	
Gly	Thr	Asn	Asn	Gln	Trp	Leu	Ala	Thr	Val	Val	Thr	Asp	Thr	Ala	Gly
			245					250						255	
Asn	Val	Thr	Ala	Pro	Asn	Val	Asp	Pro	Glu	Asn	Gln	Ala	Gly	Thr	Glu
		260				265						270			
Thr	Arg	Val	Gly	Ile	Gly	Thr	Thr	Asp	Gly	Ala	Gly	Gln	Val	Leu	Val
		275				280						285			

Gln Ala Thr Glu Asn Thr Phe Ile Val Ser Phe Asp Asn Tyr Gly His  
 290 295 300  
 Leu Ala Ser Ser Tyr Asn Val Val Gly Ala Asn Pro Asp Glu Gly Gly  
 305 310 315 320  
 Ala Pro Thr Arg His Thr Phe Asn Ile Asn Asp Gln Ser Gly Ile Ile  
 325 330 335  
 Thr Gly Val Tyr Ser Asn Gly Ala Ser Leu Glu Gly Glu Ile Gly Thr  
 340 345 350  
 Ser Arg Asn Thr Ile Thr Gln Phe Ala Glu Arg Glu Ile Gly Gln Leu  
 355 360 365  
 Ala Leu Ala Gly Phe Ala Asn Gln Gly Gly Leu Glu Lys Ala Gly Glu  
 370 375 380  
 Ser Thr Thr Lys Ala Tyr Gln Gln Asp Gly Tyr Ala Met Gly Tyr Leu  
 385 390 395 400  
 Glu Asn Phe Lys Ile Thr Tyr Ile Gln Ser Asn Asn Ser Gly Ile Ala  
 405 410 415  
 Asn Ile Thr Val Ser Gly Val Met Gly Lys Gly Lys Leu Ile Ala Gly  
 420 425 430  
 Thr Leu Glu Met Ser Asn Val Asp Leu Thr Asp Gln Phe Thr Asp Met  
 435 440 445  
 Ile Ile Thr Gln Arg Gly Phe Gln Ala Gly Ala Lys Thr Ile Gln Thr  
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 Ser Asp Thr Met Leu Glu Thr Val Leu Asn Leu Lys Arg  
 465 470 475

<210> 8

<211> 462

<212> PRT

<213> *Treponema pallidum*

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 Arg Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly  
 35 40 45  
 Phe Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln  
 50 55 60  
 Thr Thr Gly Ile Asn Thr Asp Val Ser Ile Val Asn Phe Gln Asp Leu  
 65 70 75 80  
 Ile Ser Gln Gln Leu Ser Ala Ala Ala Arg Pro Asn Glu Glu Val Gly  
 85 90 95  
 Gln Gly Ser Gly Phe Phe Val Leu Lys Ser Gly Glu Lys Thr Phe Phe  
 100 105 110  
 Thr Arg Ala Gly Ala Phe Gly Val Asp Asn Ala Gly Thr Leu Val Asn  
 115 120 125  
 Pro Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln  
 130 135 140  
 Gly Trp Met Ala Gln Asp Asp Val Ala Gly Glu Arg Leu Ile Asn Ser  
 145 150 155 160  
 Ser Ala Gln Pro Glu Leu Ala Ala Asp Ala Asn Glu Ala Asp Val Arg  
 165 170 175  
 Lys Ser Thr Gln Asp Leu Val Ile Pro Ile Gly Gln Lys Ile Asp Ala





Asn Gly Gln Phe Lys Leu Asp Glu Asn Arg Asn Leu Val Asn Met Gln  
 100 105 110  
 Gly Gln Ile Asn Leu Asn Ser Thr Asp Pro Val Met Gln Leu Thr Gly  
 115 120 125  
 Tyr Pro Ala Thr Gly Thr Pro Pro Thr Ile Gln Gln Gly Ala Asn Pro  
 130 135 140  
 Ser Lys Thr Pro Phe Ser Val Ser Asp Ala Asp Ser Tyr Asn Lys Pro  
 145 150 155 160  
 Ala Pro Ile Thr Ile Pro Asn Thr Leu Met Ala Ala Lys Ser Thr Thr  
 165 170 175  
 Thr Ala Ser Met Lys Gly Thr Val Thr Val Tyr Asp Ser Gln Gly Asn  
 180 185 190  
 Ala His Asp Met Asn Val Tyr Phe Val Lys Thr Lys Asp Asn Glu Trp  
 195 200 205  
 Ala Val Tyr Thr Gly Gly Thr Val Asn His Asp Ser Ser Asp Pro Ala  
 210 215 220  
 Ala Thr Ala Pro Ile Thr Thr Ala Ser Thr Thr Leu Lys Phe Asn  
 225 230 235 240  
 Glu Asn Gly Ile Leu Glu Ser Thr Gly Thr Ile Asn Gly Ala Thr Ala  
 245 250 255  
 Ala Thr Phe Ser Leu Ser Asn Asn Asp Gly Thr Val Val Gly Asn Tyr  
 260 265 270  
 Ser Asn Glu Gln Glu Phe Leu Asn Ser Met Gln Gln Asn Thr Gly Gln  
 275 280 285  
 Val Leu Gly Gln Ile Val Leu Ala Asn Phe Ala Asn Asn Glu Gly Leu  
 290 295 300  
 Ala Ser Gln Gly Asp Asn Asn Ile Val Ala Thr Asn Gln Asn Gly Tyr  
 305 310 315 320  
 Lys Pro Gly Asp Leu Val Ser Tyr Gln Ile Val Trp Ala Ala Thr Gln  
 325 330 335  
 Ala Ser Gly Val Ala Leu Leu Gly Thr Ala Gly Ser Gly Asn Phe Gly  
 340 345 350  
 Lys Leu Thr Asn Gly Ala Leu Glu Ala Ser Asn Val Asp Leu Ser Lys  
 355 360 365  
 Glu Leu Val Asn Met Ile Val Ala Gln Arg Asn Tyr Gln Ser Asn Ala  
 370 375 380  
 Gln Thr Ile Lys Thr Gln Asp Gln Ile Leu Asn Thr Leu Val Asn Leu  
 385 390 395 400  
 Arg

<210> 10  
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 <212> PRT  
 <213> Escherichia coli

<220>  
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 Gly Asn Asn Ile Ala Asn Ser Ala Thr Tyr Gly Phe Lys Ser Gly Thr  
 35 40 45  
 Ile Thr Gln Asp Phe Thr Asp Gly Thr Thr Thr Asn Thr Gly Thr Gly  
 50 55 60  
 Leu Asp Val Ala Ile Ala Ser Phe Ala Asp Met Phe Ala Ser Gln Asn  
 65 70 75 80  
 Gly Phe Phe Arg Leu Val Asp Ser Asn Gly Ser Val Phe Tyr Ser Arg  
 85 90 95  
 Asn Gly Gln Phe Lys Leu Asp Glu Asn Arg Asn Leu Val Asn Met Gln  
 100 105 110  
 Gly Gln Ile Asn Leu Asn Ser Ser Asp Pro Leu Leu Gln Leu Thr Gly  
 115 120 125  
 Tyr Pro Ala Thr Gly Thr Pro Pro Thr Ile Gln Gln Gly Ala Asn Pro  
 130 135 140  
 Thr Val Thr Pro Phe Ser Ala Ser Asn Ala Asp Ser Tyr Asn Lys Pro  
 145 150 155 160  
 Thr Asn Ile Ser Ile Pro Asn Thr Leu Met Ala Ala Lys Thr Thr Thr  
 165 170 175  
 Thr Ala Ser Met Lys Gly Ser Val Thr Val Phe Asp Ser Gln Gly Asn  
 180 185 190  
 Ala His Asp Met Xaa Val Tyr Phe Val Lys Thr Gly Thr Asn Gln Trp  
 195 200 205  
 Lys Val Tyr Phe Gly Ala Met Ala Asn Asn Gln Asp Ser Ser Asp Pro  
 210 215 220  
 Asn Ser Ile Ala Lys Ile Ala Thr Ala Thr Thr Leu Glu Phe Asn Ala  
 225 230 235 240  
 Asn Gly Thr Leu Val Asp Thr Gly Ala Ile Asn Gly Ala Glu Pro Ala  
 245 250 255  
 Thr Phe Ser Leu Ser Asn Asp Asp Gly Thr Val Val Gly Asn Tyr Ser  
 260 265 270  
 Asn Glu Gln Thr Phe Leu Asn Ser Met Gln Gln Asn Thr Gly Gln Leu  
 275 280 285  
 Leu Gly Gln Ile Val Leu Ala Asn Phe Ala Asn Asn Glu Gly Leu Ala  
 290 295 300  
 Ser Glu Gly Asp Asn Asn Ile Val Ala Thr Thr Gln Asn Gly Tyr Lys  
 305 310 315 320  
 Pro Gly Asp Leu Val Ser Tyr Gln Ile Val Trp Ser Ala Thr Gln Ser  
 325 330 335  
 Ser Gly Val Ala Leu Leu Gly Thr Ala Gly Thr Gly Asn Phe Gly Thr  
 340 345 350  
 Leu Thr Asn Gly Ala Leu Glu Ala Ser Asn Val Asp Leu Ser Lys Glu  
 355 360 365  
 Leu Val Asn Met Ile Val Ala Gln Arg Asn Tyr Gln Ser Asn Ala Gln  
 370 375 380  
 Thr Ile Lys Thr Gln Asp Gln Ile Leu Asn Thr Leu Val Asn Leu Arg  
 385 390 395 400

<210> 11

<211> 480

<212> PRT

<213> Aquifex aeolicus

<400> 11

Met Leu Arg Ser Phe Tyr Asn Ala Ile Thr Gly Met Asp Val Ser Arg  
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Gly Thr Val Lys Thr Thr Thr Phe Gly Ala Gly Ala Val Val Asp Ser  
20 25 30  
Phe Ala Leu Asp Val Thr Ser Asp Asn Leu Ala Asn Ala Asn Thr Val  
35 40 45  
Gly Phe Lys Lys Ser Arg Thr Gln Lys Val Trp Thr Ile Gly Ser Phe  
50 55 60  
Lys Gln Thr Glu Ile Thr Thr Asp Leu Ala Ile Pro Ile Phe Gln Asp  
65 70 75 80  
Met Val Ser Gln Val Val Val Gly Leu Asn Thr Thr Thr Glu Gly Lys  
85 90 95  
Ala Leu Phe Ile Leu Arg Asp Val Leu Thr Asn Gln Thr Tyr Tyr Thr  
100 105 110  
Arg Asp Gly Arg Phe Arg Ile Asn Arg Glu Gly Tyr Leu Ile Asn Pro  
115 120 125  
Asn Gly Pro Thr Asn Leu Asp Glu Arg Ala Pro Ile Leu Tyr Val Gln  
130 135 140  
Gly Phe Lys Val Asn Pro Val Thr Gly Glu Val Thr Gly Thr Gln Ile  
145 150 155 160  
Asp Gln Thr Thr Thr Pro Phe Asn Pro Leu Asp Ser Phe Thr Tyr Asn  
165 170 175  
Tyr Leu Glu Asp Ile Arg Val Glu Thr Gln Ile Pro Pro Lys Ala Thr  
180 185 190  
Gly Glu Ile Tyr Phe Asn Pro Arg Tyr Thr Leu Thr Ile Tyr Asp Ser  
195 200 205  
Leu Gly Arg Glu Val Pro Ala Asp Ile Tyr Phe Val Lys Thr Gly Thr  
210 215 220  
Asn Gln Trp Lys Val Tyr Phe Thr Leu Pro Thr Phe Ala Ser Lys Thr  
225 230 235 240  
Leu Glu Phe Asp Pro Ser Thr Leu Ala Ser Leu Lys Glu Arg Tyr Ile  
245 250 255  
Asn Val Asp Trp Asn Gly Asp Asp Asp Lys Gly Lys Leu Val Tyr Ile  
260 265 270  
Pro Gly Gly Asp Ile Val Gln Asp Thr Ala Asn Gln Lys Phe Tyr Leu  
275 280 285  
Thr Asp Ile Val Phe Leu Asp Leu Phe Asn Asp Gln Val His Ile Ala  
290 295 300  
Asp Asn Gly Thr Phe Ser Glu Val Asp Leu Thr Pro Glu Ser Gly Pro  
305 310 315 320  
Ser Glu Ile Asn Asp Pro Asn Asp Thr Glu Ser Tyr Leu Asn Lys Leu  
325 330 335  
Gly Ala Lys Leu Gly Ser Glu Thr Asn Lys Ile Lys Leu Ser Glu Asp  
340 345 350  
Gly Val Val Val Gly Val Tyr Ser Asn Gly Glu Thr Ile Tyr Val Gly  
355 360 365  
Glu Gly Ile Leu Gln Asn Asn Val Ile Gln Asn Ser Tyr Ile Thr Gln  
370 375 380  
His Ala Leu Pro Thr Tyr Arg Leu Ala Leu Ala Gln Phe Thr Asp Pro  
385 390 395 400  
Glu Glu Leu Val Lys Lys Gly Ser Asp Phe Val Val Thr Met Asp Gln  
405 410 415  
Asp Gly Tyr Ala Arg Gly Glu Leu Ile Asp Leu Tyr Val Leu Tyr Ala  
420 425 430

Ser Val Lys Thr Pro Thr Ile Leu Leu Pro Gly Gly Ser Asn Lys Ile  
 435 440 445  
 Arg Ser Ala Val Val Glu Met Ser Asn Val Asp Ile Ala Lys Glu Phe  
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 His His Ile Ala Asn Ala Ser Thr Tyr Gly Phe Lys Gly Ala Arg Ile  
 35 40 45  
 Ser Gln Asn Phe Asp Lys Asn Gly Ser Ile Thr Gly Thr Gly Arg Ser  
 50 55 60  
 Met Asp Leu Ala Ile Thr Glu Phe Ala Ala Val Tyr Asn Asn Gly Ser  
 65 70 75 80  
 Gly Phe Phe Val Thr Lys Asp His Met Gly Gln Thr Leu Tyr Thr Arg  
 85 90 95  
 Ser Gly Val Phe Gly Thr Asp Lys Ser Asn Phe Val Thr Ala Asn Asn  
 100 105 110  
 Gly Val Ala Asn Phe Asp Ala Ser Ala Lys Ala Ala Lys Leu Gln Gly  
 115 120 125  
 Tyr Ser Val Asp Ser Asn Asn Asn Leu Met Thr Gly Ser Ile Asp Lys  
 130 135 140  
 Ala Val Thr Pro Phe Asp Pro Ala Asp Pro Thr Ser Phe Asn Ser Val  
 145 150 155 160  
 Gly Asn Ile Gln Val Ser Thr Ser Ser Leu Asn Ala Lys Ala Thr Asp  
 165 170 175  
 Lys Leu Asp Phe Ser Tyr Thr Thr Gln Val Tyr Asp Ser Leu Gly Asn  
 180 185 190  
 Ser His Thr Val Thr Gln Tyr Phe Thr Lys Thr Ala Asp Asn Ala Trp  
 195 200 205  
 Glu Val Asn Val Pro Thr Gly Ser Phe Asn Gln Val Asp Gly Gly Lys  
 210 215 220  
 Thr Pro Val Val Ser Thr Ile Pro Val Thr Phe Asn Lys Asp Gly Thr  
 225 230 235 240  
 Leu Ala Ala Ala Phe Pro Ala Ala Gly Ala Asn Ala Met Ser Val Asp  
 245 250 255  
 Ile Asn Glu Asp Asn Gly Met Val Tyr Ala Thr Tyr Thr Asn Gly Gln  
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 Ser Leu Lys Gly Ser Thr Gln Phe Gly Ala Gln Leu Gln Gly Gln Val  
 275 280 285  
 Val Leu Ala Asp Phe Ala Asn Thr Gln Gly Leu Ala Lys Val Ser Gly  
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 Phe Gly Val Ser Thr Asn Ser Pro Asn Gly Tyr Thr Ser Gly Glu Leu  
 305 310 315 320  
 Ala Gly Val Arg Val Ala Trp Thr Gln Ser Phe Ser Ser Gly Ala Pro

325                      330                      335  
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 Ala Leu Glu Gly Ser Asn Val Asp  
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                          20                      25                      30  
 Arg Met Asp Val Val Gly Asn Asn Ile Ala Asn Val Asn Thr Ile Gly  
                          35                      40                      45  
 Phe Lys Lys Gly Arg Ile Asp Thr Ile His Thr Gln Gly Ala Phe Gln  
                          50                      55                      60  
 Ser Thr Gln Lys Ala Ser Asp Leu Gly Val Val Asn Phe Gln Asp Met  
 65                      70                      75                      80  
 Ile Ser Gln Ser Ile Ser Gly Ala Ser Arg Pro Thr Asp Ala Arg Gly  
                          85                      90                      95  
 Ser Gly Asn Gly Phe Phe Ile Leu Lys Glu Gly Phe Asn Leu Phe Tyr  
                          100                      105                      110  
 Thr Arg Ala Gly Ala Phe Asp Val Asp Ser Asp Arg His Leu Val Asn  
                          115                      120                      125  
 Pro Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Ile Gln  
                          130                      135                      140  
 Gly Trp Met Ala Arg Asp Leu Glu Gly Glu Lys Val Ile Asn Thr Ala  
 145                      150                      155                      160  
 Ser Asp Pro Leu Ile Gln Glu Gly Ala Asn Pro Ala Asp Ile Ala Arg  
                          165                      170                      175  
 Gly Ile Glu Asp Leu Ile Ile Pro Ile Gly Asp Lys Glu Gly Ala Lys  
                          180                      185                      190  
 Ser Thr Lys Lys Val Thr Phe Thr Trp Val Val Asn Lys Ser Leu Tyr  
                          195                      200                      205  
 Asp Ser Phe Gly Asn Val Ser Val Leu Glu Leu Arg Val Val Lys Asp  
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 Leu Asn Thr Pro Asn Leu Trp Asn Ala Thr Val Leu Asn Gly Gln Pro  
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 Gly Gln Lys Leu Ile Asn Gly Glu Gln Asn Gly Asp Ile Leu Gln Ile  
                          245                      250                      255  
 Pro Ile Ser Asn Phe Thr Leu Gly Phe Asp Asn Glu Gly Ala Leu Ala  
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 Ser Thr Phe Asn Val Leu Gly Ala Asn Val Thr Glu Val Gly Glu Thr  
                          275                      280                      285  
 Gln Thr Val Asn Leu Lys Asp Gln Asp Gly Val Ile Val Gly Ile Tyr  
                          290                      295                      300  
 Ser Asn Gly Ile Arg Leu Gly Thr Val Gly Ser Tyr Thr Asp Ser Ile  
 305                      310                      315                      320  
 Thr Gln Phe Ala Asp Arg Asp Leu Gly Lys Ile Ala Leu Ala Ser Phe  
                          325                      330                      335

Met	Asn	Pro	Gly	Asp	Leu	Gln	Asn	Gln	Ala	Ile	Ser	Ser	Thr	Lys	Ala
			340					345					350		
Ile	Ile	Gln	Asp	Gly	Tyr	Gly	Met	Gly	Tyr	Met	Glu	Asn	Tyr	Glu	Ile
		355					360					365			
Ile	Leu														
	370														